What is claimed is:

1. A method for identifying loss of imprinting of the IGF2 gene in a subject, comprising analyzing a biological sample from the subject for hypomethylation of a differentially methylated region (DMR) of at least one of the H19 gene and the IGF2 gene.

2. The method of claim 1, wherein the method comprises analyzing the biological sample for hypomethylation of a DMR of the IGF2 gene comprising SEQ ID NO:1 or a polymorphism thereof, or a fragment of SEQ ID NO:1 or a polymorphism thereof.

3. The method of claim 1, wherein the method comprises analyzing the biological sample for hypomethylation of a DMR of the H19 gene comprising SEQ ID NO:6 or a polymorphism thereof, or a fragment of SEQ ID NO:6 or a polymorphism thereof.

4. The method of claim 1, wherein the method comprises analyzing the biological sample for hypomethylation of both a DMR of the H19 gene and a DMR of the IGF2 gene.

5. The method of claim 2, wherein the DMR of the IGF2 gene comprises SEQ ID NO:1.

6. The method of claim 3, wherein the DMR of the H19 gene comprises SEQ ID NO:6.

7. The method of claim 3, wherein the H19 DMR comprises a CTCF binding site.

8. The method of claim 3, wherein the analysis is performed by contacting the biological sample with a primer pair comprising at least one pair of:

SEQ ID NO:7 and SEQ ID NO:8;

SEQ ID NO:9 and SEQ ID NO:10;

SEQ ID NO:11 and SEQ ID NO:12,

SEQ ID NO:13 and SEQ ID NO:14;

SEQ ID NO:15 and SEQ ID NO:16;
SEQ ID NO:17 and SEQ ID NO:18;
SEQ ID NO:19 and SEQ ID NO:20;
SEQ ID NO:21 and SEQ ID NO:22.
SEQ ID NO:23 and SEQ ID NO:24;
SEQ ID NO:25 and SEQ ID NO:26;
SEQ ID NO:31 and SEQ ID NO:32; and
SEQ ID NO:33 and SEQ ID NO:34.

9. The method of claim 2, wherein the analysis is performed by contacting the biological sample with a primer pair comprising at least one pair of:
SEQ ID NO:2 and SEQ ID NO:3;
SEQ ID NO:4 and SEQ ID NO:5;
SEQ ID NO:27 and SEQ ID NO:28; and
SEQ ID NO:29 and SEQ ID NO:30.

10. A method for identifying an increased risk of developing cancer in a human subject, comprising analyzing a biological sample from the subject for hypomethylation of a differentially methylated region (DMR) of an H19 gene or an IGF2 gene.

11. The method of claim 10, wherein the cancer is colorectal cancer.

12. The method of claim 10, wherein the methods comprises bisulfite genomic sequencing performed using the primer pair SEQ ID NO:23 and SEQ ID NO:24, followed by the primer pair SEQ ID NO:25 and SEQ ID NO:26.

13. The method of claim 10, wherein the subject is not a subject known to have a colorectal neoplasm.

14. The method of claim 10, wherein the H19 DMR comprises SEQ ID NO:6 or a polymorphism thereof, or a fragment of SEQ ID NO:6 or a polymorphism thereof and the IGF2 DMR corresponds to SEQ ID NO:1 or a polymorphism thereof, or a fragment of SEQ ID NO:1 or a polymorphism thereof.

15. The method of claim 10, wherein the method comprises analyzing the biological sample for hypomethylation of a differentially methylated region (DMR) of an H19 gene and an IGF2 gene.

16. The method of claim 10, wherein the biological sample is a blood sample.

17. A method for identifying an increased risk of developing cancer in a subject, comprising analyzing a first biological sample from the subject for loss of imprinting of the IGF2 gene, wherein a loss of imprinting of the IGF2 gene is indicative of an increased risk of developing cancer, thereby identifying an increased risk of developing cancer in the subject.

18. The method of claim 17, wherein the cancer is colorectal cancer.

19. The method of claim 17, wherein the method comprises analyzing genomic DNA from the biological sample for hypomethylation of one or both of the H19 gene and the IGF2 gene.

20. The method of claim 19, wherein hypomethylation is analyzed for at least one of an H19 DMR comprising SEQ ID NO:6 or a polymorphism thereof, or a fragment of SEQ ID NO:6 or a polymorphism thereof, and an IGF2 DMR comprising SEQ ID NO:1 or a polymorphism thereof, or a fragment of SEQ ID NO:1 or a polymorphism thereof.

21. A kit for determining a methylation status of a differentially methylated region (DMR) of IGF2 or H19, comprising one or more primer pairs corresponding to one or more of:

SEQ ID NO:2 and SEQ ID NO:3,

SEQ ID NO:4 and SEQ ID NO:5,

SEQ ID NO:23 and SEQ ID NO:24,

SEQ ID NO: 25 and SEQ ID NO:26,

SEQ ID NO:27 and SEQ ID NO:28, and

SEQ ID NO: 29 and SEQ ID NO:30.